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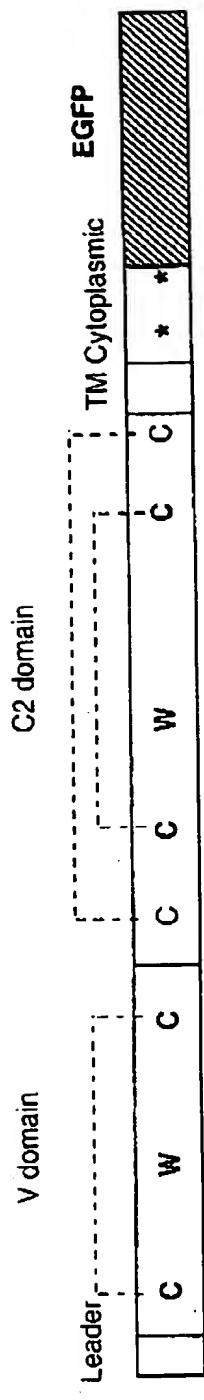
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ACAGGACCCGCCCTCTGCTTCCACCTCTAGGGACCTCCTCTGCTCCGGCCGGGGAAGTGTGGAGACCCAGCCG  
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ACCGTCAAGAAGTCACAGTAATAGAGTTCCAGAGGGCTATTGGCTGTGTAACACCCAAAGAAGACTACCTCTCCAGA  
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TGGAGTGTAGATTCTAACATACGAATCAAAATGTTACAAGAAGTGTGCTGGAGAGTATCGTGTGAAAGTCAAGGCTC  
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CaCCGGAGTGGCCCTGGGAAGGCAAGTCAAGTGAAGTGAAGTGTCTCAACATAAGGCCCATCATAGAACCGTTGTGGTGG  
CTTCGTGATTCTGTaTGTGGCCTGGCACATGCTATGCTCAGAGGAAAGGCTACTTTCAAAAGAAACTCTCTCCAGA  
AGGGCAGTCTGCACTAAAGTCACTACGATGgGCGAAATGATTCTGAGCACAACATGTTTAAAGAAT  
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ATGAAGAAATATGAAAGGGGAGTTCTACAGAAGTTTATGATCTCAACTACAAAGAAATTTTAAAGCAGGAAAGCTT  
GCCATCAATTACACCTGGCATCTGTGTGACCTAAAGGAAATGCTGTGATTATCTGGTTTGTGAAGGCCAAAT  
GAATGTCAAGTTGGAGTTGACTATACACACTGACTGTAAAGGCTAATCCAAGAAGCAAGAAATAAAAA  
AAAAAAAAAAAAAAAAAAAAAATTTC

Fig. 1



**JAM-EGFP**  
**CRAM-1-EGFP**  
**CRAM-2-EGFP**

**QPS<sub>285</sub>-EGFP**  
**DGV<sub>291</sub>-EGFP**  
**KVT<sub>283</sub>-EGFP**

**Tac Leader**      **Tac TM**

**Tac**

**Tac-W<sub>258</sub>FAY....**  
**Tac-C<sub>264</sub>CAY....**  
**Tac-C<sub>259</sub>YAQ....**

**Tac-JAM**  
**Tac-CRAM-1**  
**Tac-CRAM-2**

**Fig 2-1**

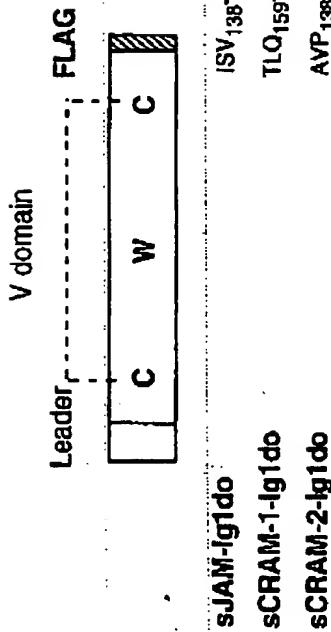
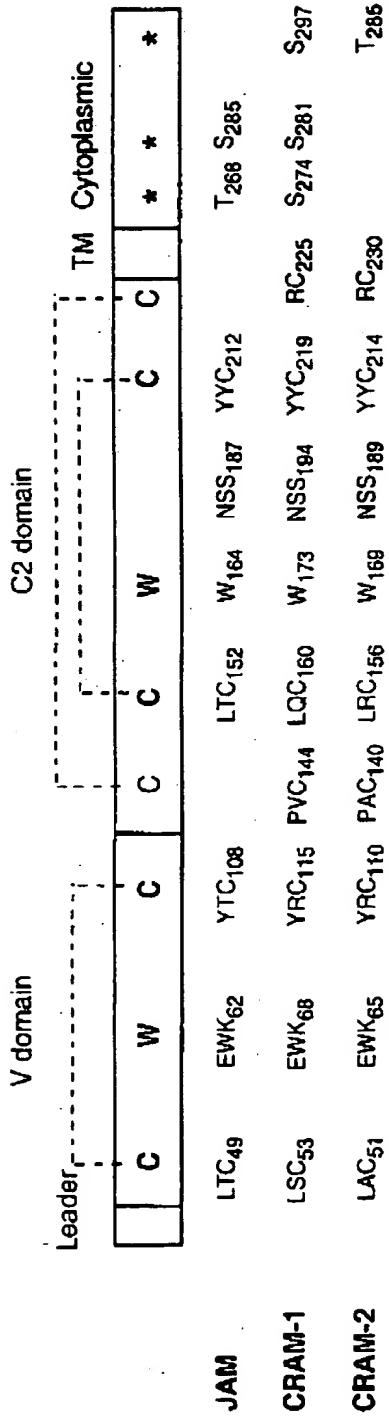
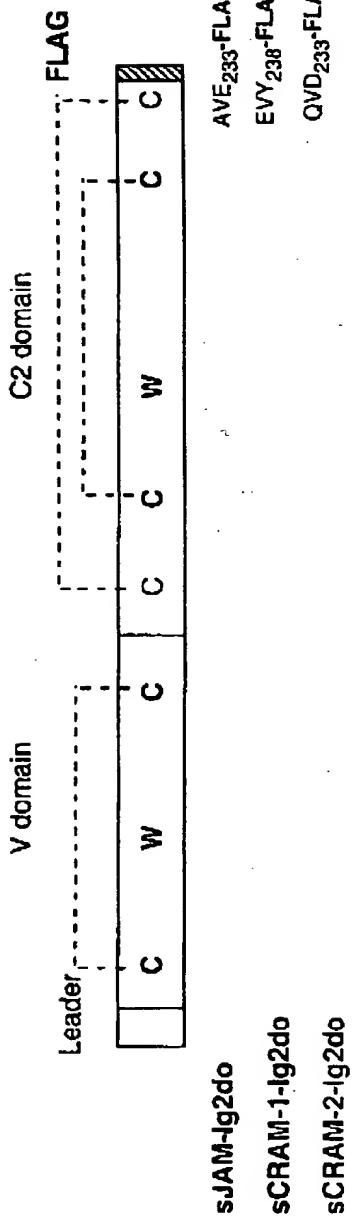


Fig 2-2



MALSRRRLRLR LYARLPHFFL LLLFRGCMIE AVNLKSSNRM PVVHEFESVE  
MARSFQGL LMLLLHYLI VALDYHKANG FSASKDHRQE VTVIEFQEAI

LSCIITHSQT SDPRIEWKKI QDGQTTYVYF DNKIQGDLAG RTDVFGKTS  
LACK-TPKKT TSSRLEWKV GQG-VSLVYY QQALQGDFKD RAEMID-FNI

RIWNVTRSDS AIYRCEVVAL NDR-KEVDEI TIELIVQVKP VTPVCRIPAA  
RIKNVTRSDA GEYRCEVSAP TEQGQNLQED KVMLEVLVAP AVPACEVPTS

VPVGKTATLQ CQESEGYPRP HYSWYRNDVP LPT-DSRANP RFQN88FHVN  
VMTGSVVELR CQDKEGNPAP EYIWFKDGT S LLG-NPKGGT H-NNSSYTNE

SETGTLVFNA VHKKDSGQYY CIA8NDAGAA RCEGQDMEVY DLNIAGIIGG  
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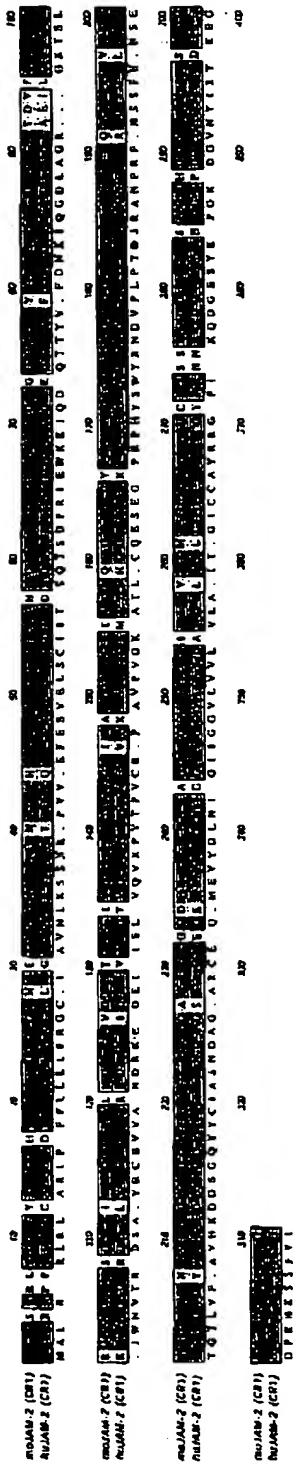
VLVVLIVLAV ITMGICCAYR RGCFISSLQD GESYKSPGKH DGVNYIRTSE  
VVVVAFVISV CGLGTCYAQR KGYF--SKET SFQKGSPASK -----VTTMG

EGDFRHKS8F VI  
ENDFRHTKSF II

Fig 3

Fig 4

Murine and human JAM-2 (CRAM-1)



Murine and human CRAM-2 (JAM-3)

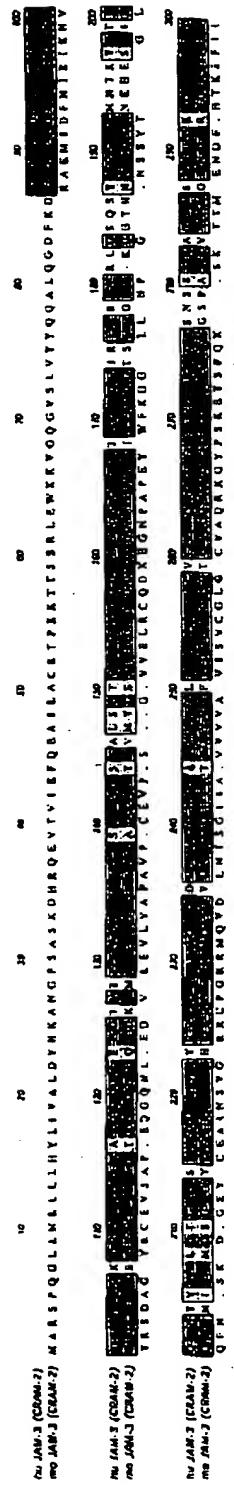


Fig 5

## &gt; Nucleic acid sequence huCRAM-1/huJAM-2

ATGGCGCTGAGGCGGCCACCGCGACTCCGGCTCTGCCTCGGCTGCCTGACTTCTTCCT  
 GCTGCTGCTTTCAGGGCTGCCATAGGGGCTGTAAATCTCAAATCCAGCAATCGAA  
 CCCCAGTGGTACAGGAATTGAAAGTGTGGAACTGTCTGCATCATTACGGATTGCAG  
 ACAAGTGACCCAGGATCGAGTGAAGAAAATTCAAGATGAACAAACCACATATGTGTT  
 TTTGACAAACAAAATTCAAGGGAGACTTGGCGGGCTGAGAATACTGGGGAAGACAT  
 CCCTGAAGATCTGGAATGTGACACGGAGAGACTCAGCCCTTATCGCTGTGAGGTCGTT  
 GCTCGAAATGACCGCAAGGAAATTGATGAGATTGTGATCGAGTTAACTGTGCAAGTGAA  
 GCCAGTGACCCCTGTCTGTAGAGTGCCGAAGGCTGTACCAAGTAGGCAAGATGGCAACAC  
 TGCAGTGCCAGGAGAGTGAGGGCCACCCCCGGCCTCACTACAGCTGGTATCGCAATGAT  
 GTACCACTGCCACGGATTCCAGAGCCAATCCCAGATTGCAATTCTTCCACTT  
 AAACTCTGAAAACAGGCACTTGGTGTCACTGCTGTACAGGACGACTCTGGGCACT  
 ACTACTGCATTGCTTCAATGACCCAGGCTCAGCCAGGTGTGAGGAGCAGGAGATGGAA  
 GTCTATGACCTGAACATTGGCGGAATTATTGGGGGGTTCTGGTTGCTCTGCTGTACT  
 GGCCCTGATCACGTTGGCATCTGCTGTGACATACAGACGTGGTACTTCATCAACAATA  
 AACAGGATGGAGAAAGTTACAAGAACCCAGGGAAACCAGATGGAGTTAACTACATCCGC  
 ACTGACGAGGAGGGCGACTTCAGACACAAGTCATCGTTGTGATCTGAGACCCGGTGT  
 GGCTGAGAGCGCACAGAGCGCACGTGCACATACCTCTGCTAGAAAACCTCTGCAAGGC  
 AGCGAGAGCTGATGCACTCGACAGAGCTAGACACTCTCAAAGCTTTCGTTGGCAAG  
 GTGACCACTACTCTTTACTCTACAAGCCATGAAAAGAGAAATTTCATCAAGAGGACC  
 CGGAAATATAACCCAAGGAACCAAATGGGTGCGTCACTGAGGTGGGTCTTAATT  
 TGTTTTGGCTGATTCCATGAAAATAAGGGGTCTTAAGAGTTGGTACGTAAAACC  
 CCCCGCTTGGCCTTGGAAACCACATGTTACCACTGCCTTAAAAA

## &gt; huCRAM-1/huJAM-2 complete

MALRRPPRLRLCARLPDF~~LLL~~FRGLIGAVNLKSSNRTPVVQE~~F~~VELSCIITDSQ  
 TSDPRIEWKKIQDEQTTYVF~~DN~~KIQGDLAGRAEILGKTS~~LN~~KIWNVTRRDSALYRCEVV  
 ARNDRKEIDEIVIELTVQVKPVT~~P~~VCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRND  
 VPLPTDSRANPRFRNSSF~~H~~LNSETGTLVFTAVHKDDSGQYYC~~I~~ASNDAGSARCEEQEME  
 VYD~~L~~NINGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGE~~S~~YKNPGKPDGVNYIR  
 TDEEGDFRHKSSFVI

## &gt;huCRAM-2/huJAM-3 partial

RAEMIDFNIRIKNVTRS~~D~~AGK~~Y~~RCEVS~~A~~PAEQGQNLEEDTVTLEV~~V~~APAVPSCEVPSS  
 ALSGT~~V~~VELRCQDKEGNPAPEYTWFKDGIRLLEN~~P~~RLGSQ~~S~~TMNTKTGTLQFNT  
 VSKLDTGEYSCEARN~~S~~VG~~Y~~RRCPGKRMQV~~D~~DLNISGIIAAVVV~~V~~VALVIS~~V~~CG~~L~~GV~~C~~Y~~A~~Q  
 RKGYFSKETSFQKS~~N~~SSSKATTMSE~~N~~DFKHTKS~~F~~II

Fig 6

**A**

Y R C X A S1  
TAY AGN TGY NNN GCY TCY AA

Y R C X A S2  
TAY AGN TGY NNN GCY AGY AA

Y Q C X A S1  
TAY CRG TGY NNN GCY TCY AA

Y Q C X A S2  
TAY CRG TGY NNN GCY AGY AA

Y Y C X A S1  
TAY TAY TGY NNN GCY TCY AA

Y Y C X A S2  
TAY TAY TGY NNN GCY AGY AA

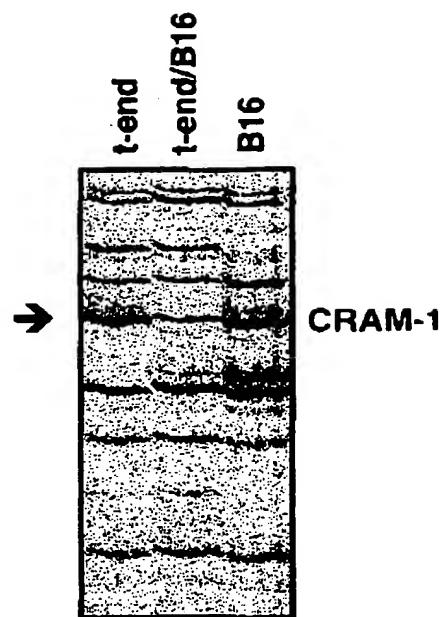
**B**

Fig 7

A

gacatccccctcgacatggcgctgagccggcggtgcgacttcgactgtacgcgggttg  
 M A L B R R L R L Y A R L  
 cctcaacttccctgtgtcttccatggggctgcatgatagaggcgtgaatctccaa  
 P R P P L L L L R G C M I E A V N L K  
 tccagcaaccgaaaccctggatgtacatgaaatgtgaaatgtgtggaaattgtcttcatt  
 S S N R N P V V H E F E S V E L S (C) I I  
 acgcaactcacaagacaatgtgacccttaggatgtaaatggaaatccaaatggccaaacc  
 T B S Q T S D P R I E W K K I Q D G Q T  
 acatatgtgtatgttgcacaaatggacaggagatctggcgggtgcacatgtgttt  
 T Y V Y P D N R I O G D L A G R T D V F  
 ggaaaaacttccctgaggatgtggatgtggatgtggatgtggatgtggatgtggatgt  
 G K T S L R A I W E T R S D S A I Y R (C)  
 gaggtcggt  
 E V A L S D R K E V D R I T I E L I V  
 caagtgaacccatgtgaccctgtctgcggatattccacggatgttgcacatgtggacag  
 Q V K P V T F V C R I F A V F V G K T  
 gcaacactgtggccaaatggacggcgggtatcccgccctactacatgtggatgg  
 A T L Q (C) Q E S E G Y P R F H Y S W Y R  
 aatgtatgtggccactgt  
 N D V F L P T D S R A N P R F Q H S S F  
 catgt  
 H V N S E T C T L V F N A V E K D D S G  
 cgtactactgt  
 Q Y (C) I A S N D A G A A R C B G Q D M  
 gaagtgtatgtatgt  
 E V Y D L N I A G I I G G V L V V L I V  
 cttgt  
 L A V I T M G I C C A Y R R G C F I S g  
 aaacaagatggaaatgtataagagccccaggaaagcatgacgggttaactacatccgg  
 K Q D G E B S Y K S F G R K B D G V N Y I R  
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 F S E G D P R H K S S F V I  
 gggagagcacatgtcaactgtgtggaaatgtgtgtgtgtgtgtgtgtgtgtgt  
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 ttcoaatctaaaaaaa 1980

B

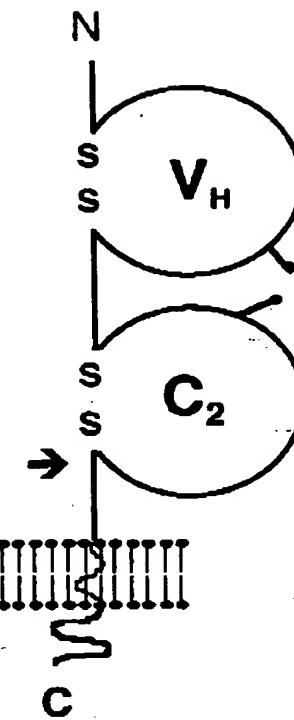


Fig 8

		20	40	60	80	100
CRAM-1	MASSIRRLRIVAYATPENRQGQI	FRGCRCIEAVNEPESNRPVWPFESVE	IIIWQJDEI	RIGDDEQYI	LEFDNK	YDVEGKTS
CRAM-2	NAPSPOEFLQHIL	DIYHKANPFSASHDHOEEL	AKTPEKKLSS	LYQQA	QDDEKQ	AEMID-FN
JAM	NGTERAGRKILH	LGSLVQCKGVIQAQSDQ	FECAIAK	VSE	95	93
Consensus	EL	EL	EL	EL	EL	EL
CRAM-1	ESAI R F VELNDR-KED	ELDIDELI	QKVVIVVERI	ANPV	KETQ	ANPQ
CRAM-2	REKKA	ELDIDELI	QKVVIVVERI	ANPV	QES	YH
JAM	TESS	ELDIDELI	QKVVIVVERI	ANPV	QES	YH
Consensus	EL	EL	EL	EL	EL	EL
CRAM-1	SE	TY	EL	EL	EL	EL
CRAM-2	H2	TY	EL	EL	EL	EL
JAM	PK	TY	EL	EL	EL	EL
Consensus	EL	EL	EL	EL	EL	EL
		200	400	600	800	1000
CRAM-1	120	140	160	180	200	220
CRAM-2	120	140	160	180	200	220
JAM	120	140	160	180	200	220
Consensus	120	140	160	180	200	220
CRAM-1	240	260	280	300	320	340
CRAM-2	240	260	280	300	320	340
JAM	240	260	280	300	320	340
Consensus	240	260	280	300	320	340

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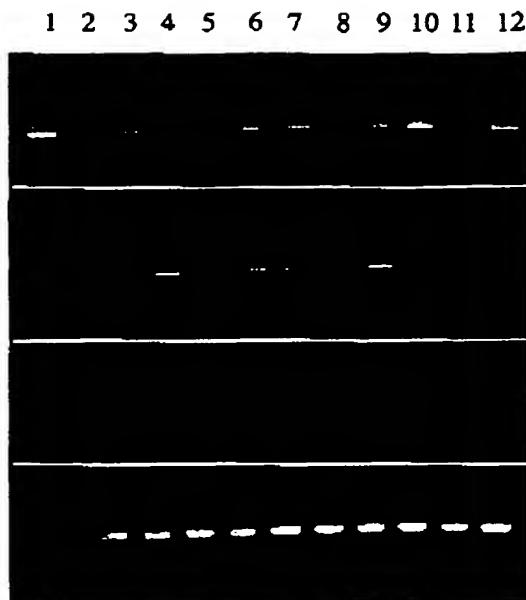
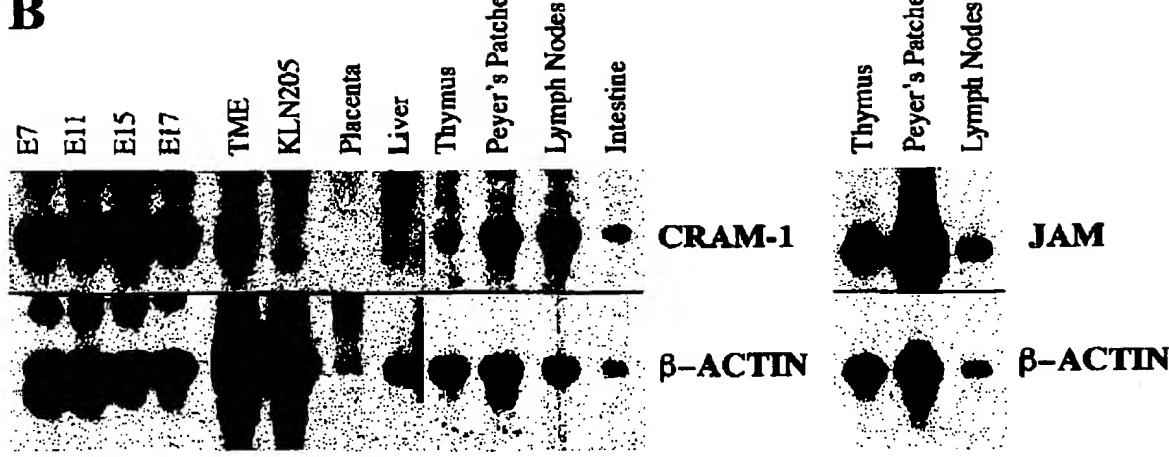
**A****JAM****CRAM-1****CRAM-2****HPRT**

Fig 10

**B****CRAM-1****JAM** $\beta$ -ACTIN $\beta$ -ACTIN

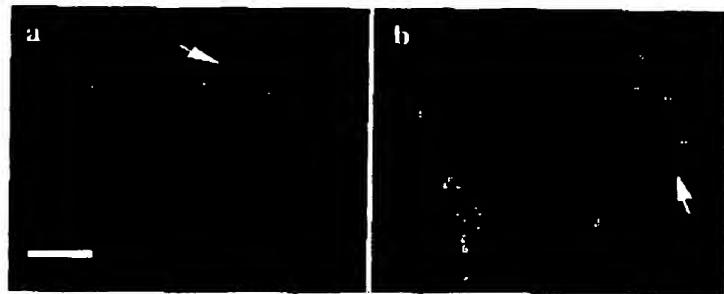
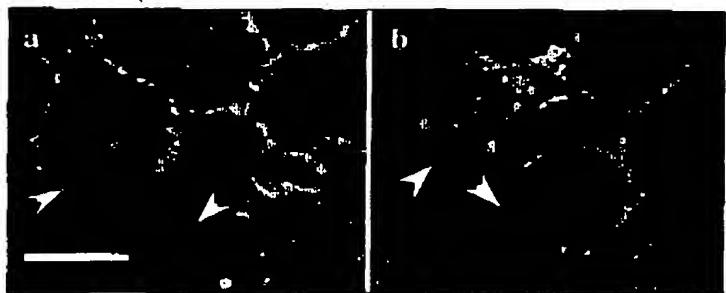
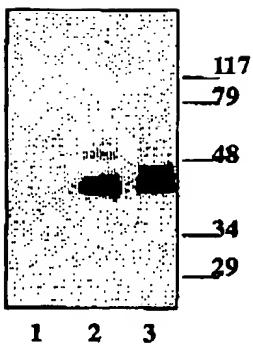
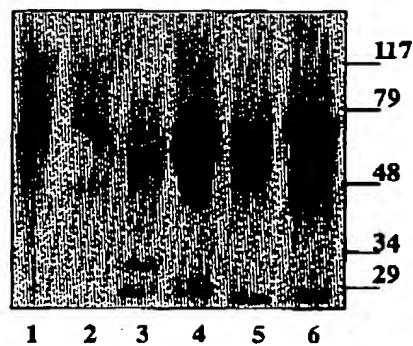
**A****B****C****D**

Fig 11

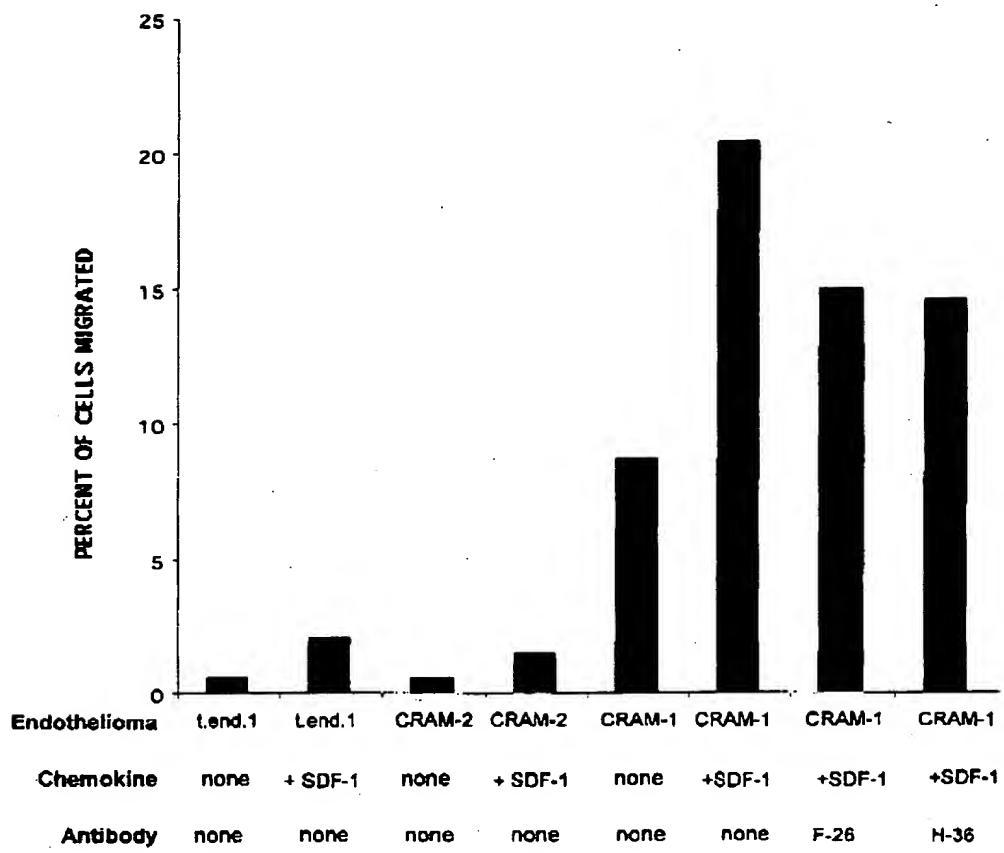


Fig 12

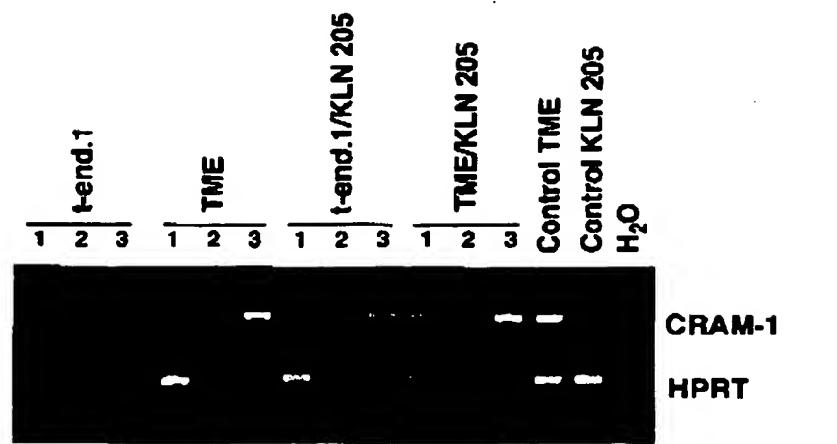


Fig 13

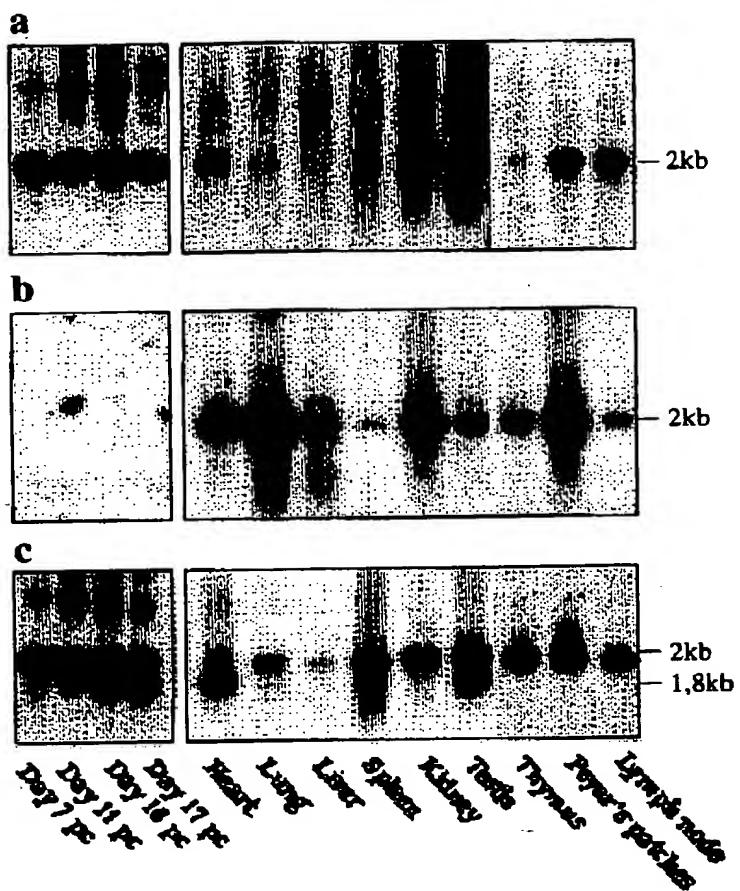


Fig 14

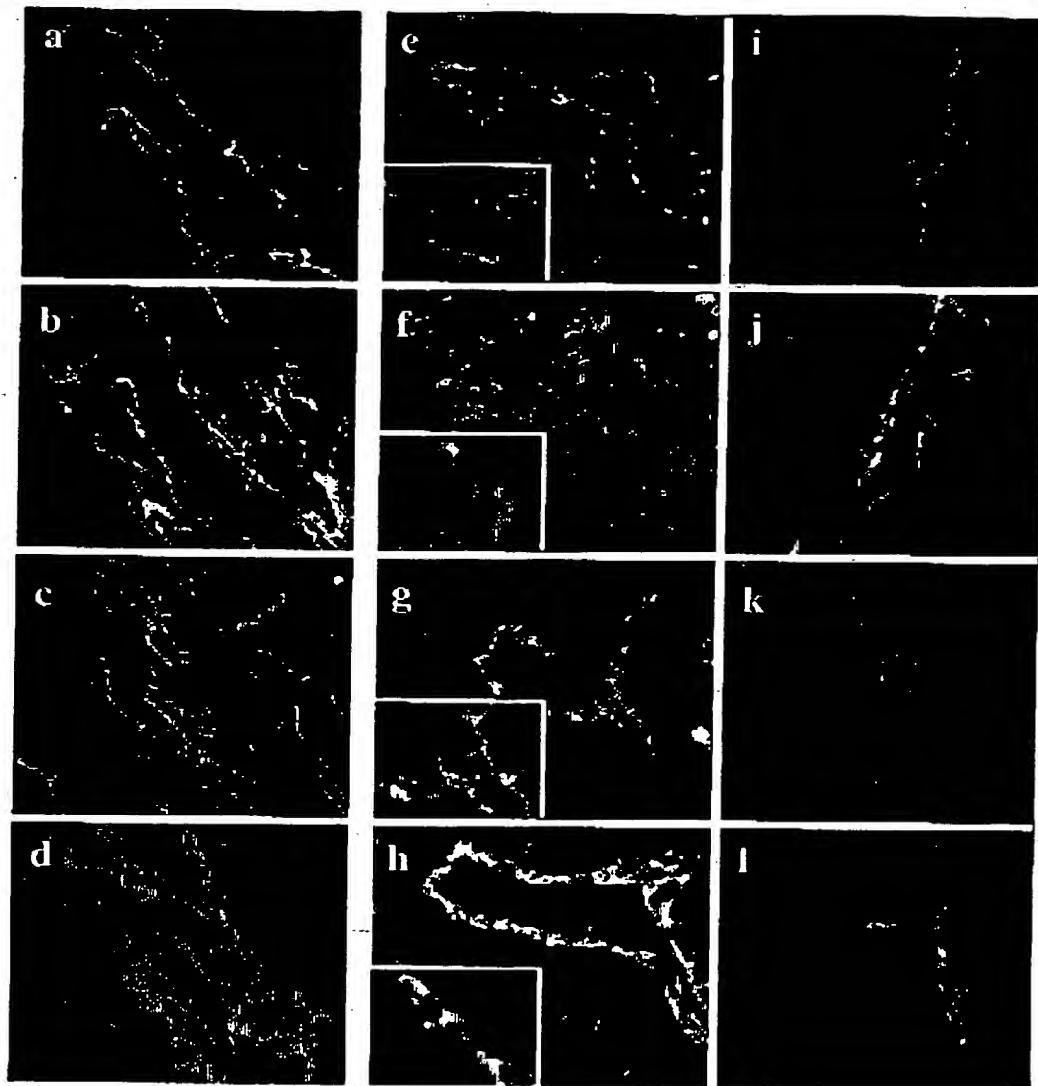


Fig 15

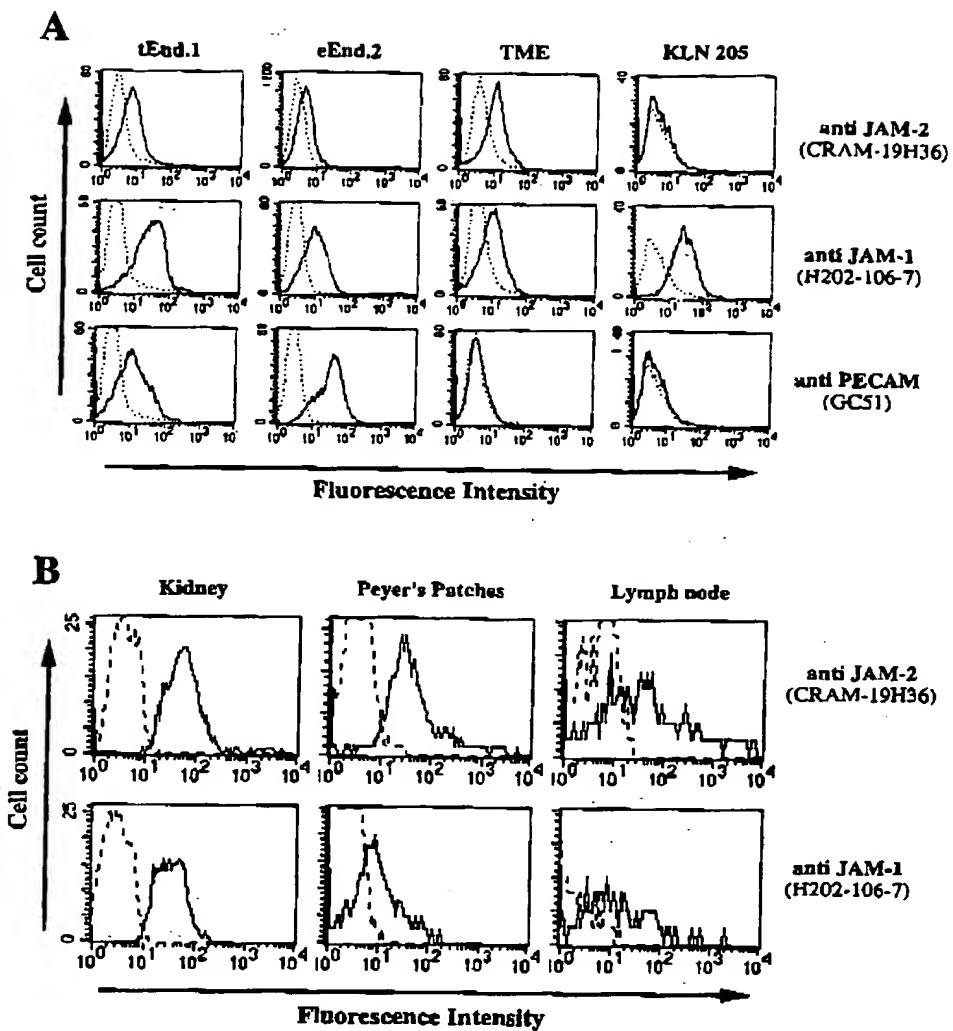
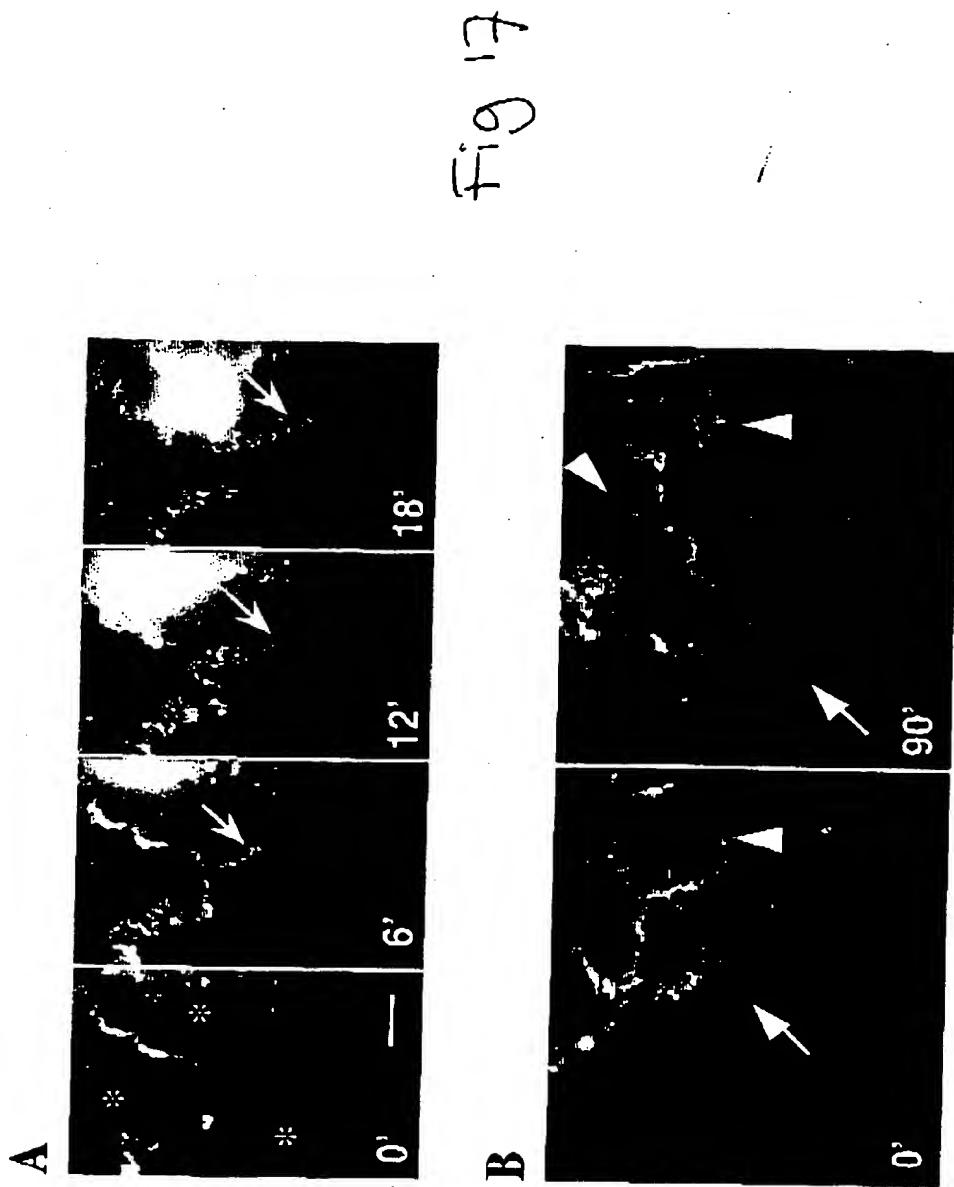


Fig 16



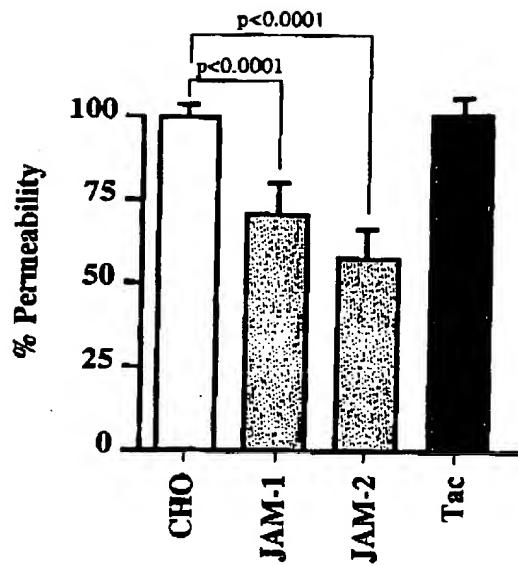
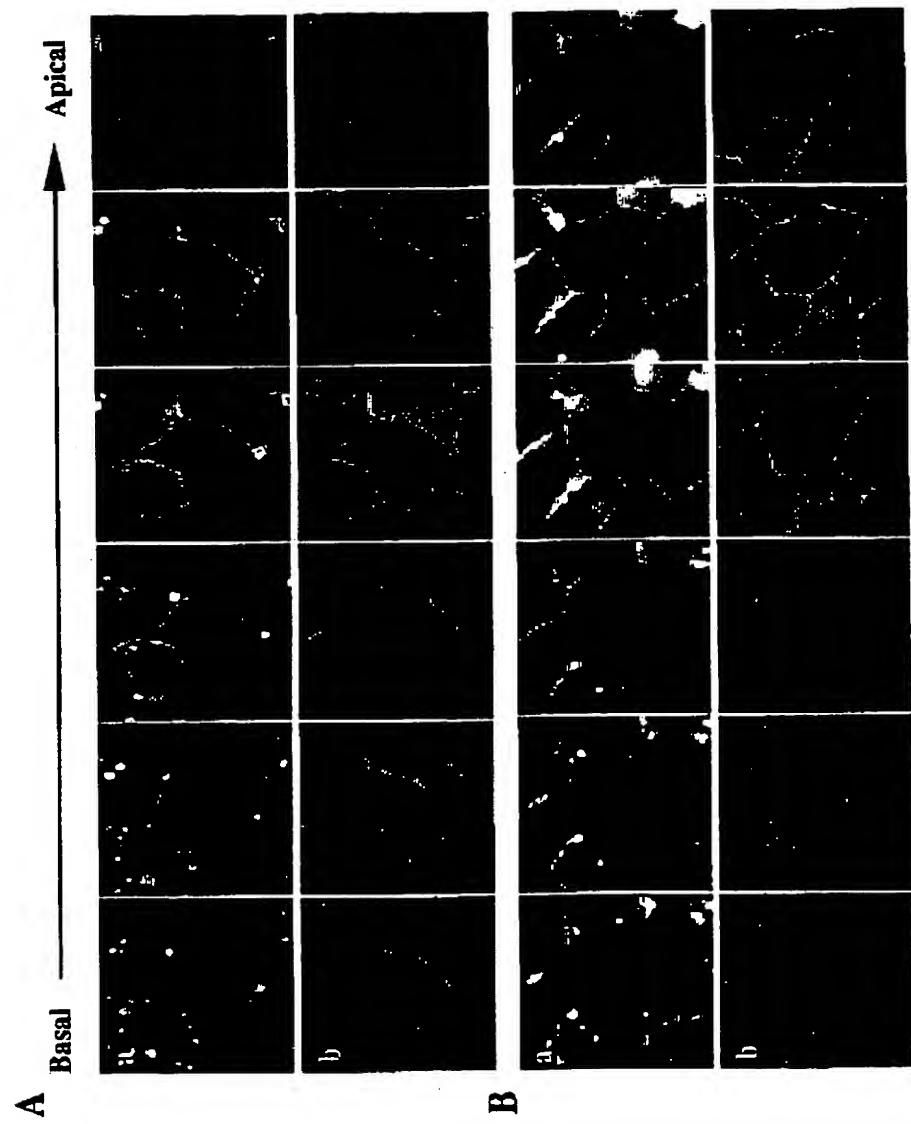
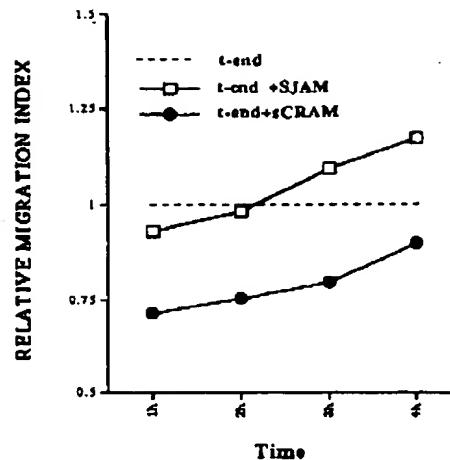


Fig 1B

Fig 19



A



B

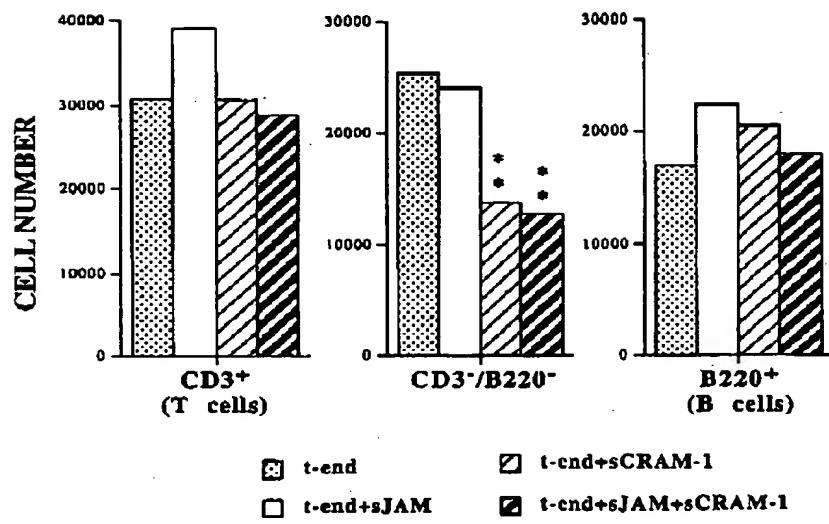


Fig 20